Amendments to the Claims:

This listing of claims will replace all prior versions and listings of claims in the application:

Listing of Claims

1. (original) An isolated DNA molecule comprising the nucleotide sequence of SEQ ID NO:1.

2. (previously presented) An isolated DNA molecule comprising at least 24 contiguous nucleotides selected from nucleotides 1-1532 of SEQ ID NO:2, wherein the DNA molecule has transcriptional regulatory activity.

3. (previously presented) An isolated DNA molecule comprising the nucleotide sequence consisting of nucleotides 1533-4700 of SEQ ID NO:2.

4. (previously presented) The isolated DNA molecule of claim 3 comprising the nucleotide sequence consisting of nucleotides 1-4700 of SEQ ID NO:2.

Claims 5-6 (cancelled)

7. (previously presented) An isolated DNA molecule comprising a nucleotide sequence that hybridizes to nucleotides 1-1532 of SEQ ID NO:2 or a complement thereof, wherein hybridisation conditions comprise hybridisation in 6x SSC, 20 mM Na_2HPO_4, 0.4% SDS, 500 μg/ml Salmon sperm DNA at 65°C for 20 hours, followed by a wash with 2x SSC, 0.5% SDS at 20°C, and a wash at 65°C with 0.1x SSC, 0.5% SDS, wherein the nucleotide sequence has transcriptional regulatory activity.

8. (original) The isolated DNA molecule of claim 7, comprising the nucleotide sequence of nucleotides 1-1532 of SEQ ID NO:2.

9. (previously presented) An isolated DNA molecule comprising at least 32 contiguous nucleotides selected from nucleotides 1752-2382 of SEQ ID NO:2, wherein the DNA molecule has transcriptional regulatory activity.

10. (previously presented) The isolated DNA molecule of claim 9 comprising nucleotides

1752-2382 of SEQ ID NO:2.

11. (previously presented) An isolated DNA molecule comprising at least 23 contiguous nucleotides selected from nucleotides 2575-3604 of SEQ ID NO:2, wherein the DNA molecule has transcriptional regulatory activity.

12. (previously presented) The isolated DNA molecule of claim 11 comprising nucleotides 2575-3604 of SEQ ID NO:2.

13. (previously presented) An isolated DNA molecule comprising at least 22 contiguous nucleotides selected from nucleotides 3770-4032 of SEQ ID NO:2, wherein the DNA molecule has transcriptional regulatory activity.

14. (previously presented) The isolated DNA molecule of claim 13 comprising nucleotides 3770-4032 of SEQ ID NO:2.

15. (original) A vector which comprises the DNA molecule of claim 1.

16. (original) A vector which comprises the DNA molecule of claim 2.

17. (original) A vector which comprises the DNA molecule of claim 3.

18. (original) The vector of claim 16 which comprises a heterologous gene of interest under control of the DNA molecule.

19. (previously presented) A host cell expressing the DNA molecule within the vector of claim 15.

20. (previously presented) A transgenic seed coat cell expressing a gene of interest under control of a regulatory region, wherein the gene of interest and regulatory region are contained within the vector of claim 16.

21. (previously presented) A host cell expressing the DNA molecule within the vector of claim 17.

22. (previously presented) A transgenic seed coat cell expressing the DNA molecule within the

vector of claim 18.

23. (original) A transgenic plant comprising the vector of claim 15.

24. (previously presented) A transgenic soybean plant comprising the vector of claim 16.

25. (original) A transgenic plant comprising the vector of claim 17.

26. (previously presented) A transgenic soybean plant comprising the vector of claim 18.

27. (previously presented) A method for the production of soybean seed coat peroxidase in a host comprising:

i) transforming the host with a vector comprising the isolated DNA molecule as defined in claim 1 operably linked with a regulatory region; and

ii) culturing the host under conditions to allow expression of the soybean seed coat peroxidase.

28. (previously presented) A process for producing a heterologous gene of interest in a transgenic soybean plant comprising, transforming the transgenic soybean plant with the heterologous gene of interest under control of a regulatory region, the heterologous gene of interest and the regulatory region contained within the vector of claim 16, and growing the transgenic plant under conditions to allow expression of the heterologous gene of interest.

29. (original) The process of claim 28 wherein the heterologous gene of interest is produced within seed coat cells.

30. (previously presented) A vector comprising the DNA molecule of claim 7.

31. (previously presented) A process for producing a heterologous gene of interest in a transgenic soybean plant comprising, transforming the transgenic soybean plant with the heterologous gene of interest under control of a regulatory region, the heterologous gene of interest and the regulatory region contained within the vector of claim 30, and growing the transgenic plant under conditions to allow expression of the heterologous gene of interest.

32. (previously presented) An isolated DNA molecule comprising at least 20 contiguous nucleotides selected from nucleotides 1524-1610 of SEQ ID NO:2, wherein the DNA molecule has transcriptional regulatory activity.

33. (previously presented) The isolated DNA molecule of claim 32 comprising nucleotides 1524-1610 of SEQ ID NO:2.

Claims 34-35 (cancelled)

36. (previously presented) A method of selecting between an EpEp and an epep plant genotype comprising the steps of:

a) preparing genomic DNA, or cDNA from a plant;

b) fragmenting the genomic DNA or cDNA to produce DNA fragments;

c) separating the DNA fragments;

d) hybridizing the fragments with a labelled nucleotide sequence, where the nucleotide sequence is the isolated DNA molecule defined in claim 32, to produce a hybridization pattern; and

e) determining whether the hybridization pattern is representative of an EpEp or an epep genotype.

37. (previously presented) A method of selecting between an EpEp and an epep plant genotype comprising the steps of:

a) preparing genomic DNA, or cDNA from a plant;

b) fragmenting the genomic DNA or cDNA to produce DNA fragments;

c) amplifying the DNA fragments using at least one primer, the at least one primer comprising the isolated DNA molecule defined in claim 32 to produce an amplified product; and

e) determining whether the amplified product is representative of an EpEp or epep genotype.

38. (previously presented) A method of selecting a soybean plant having a deletion in a peroxidase gene, which method comprises the steps of:

a) preparing genomic DNA, or cDNA from a plant;

b) fragmenting the genomic DNA or cDNA to produce DNA fragments;

c) separating the DNA fragments;

d) hybridizing the fragments with a labelled nucleotide sequence, where the nucleotide sequence is the isolated DNA molecule defined in claim 32, to produce a hybridization pattern; and

e) determining whether the hybridization pattern is representative of an EpEp genotype or a genotype of a soybean plant having a deletion in a peroxidase gene.

39. (previously presented) A method of selecting a soybean plant having a deletion in a peroxidase gene, which method comprises the steps of:

a) preparing genomic DNA, or cDNA from a plant;

b) fragmenting the genomic DNA or cDNA to produce DNA fragments;

c) amplifying the DNA fragments using at least one primer, the at least one primer comprising the isolated DNA molecule defined in claim 32 to produce an amplified product; and

e) determining whether the amplified product is representative of an EpEp genotype or a genotype of a soybean plant having a deletion in a peroxidase gene.

Claim 40 (cancelled)